REMARKS

Claims 1, 2, 4-7, 9, and 10 are pending in the present application.

The rejection of Claims 1-3 under 35 U.S.C. §112, first paragraph (enablement), is obviated in part by amendment and traversed in part.

The Office has taken the position that the claimed invention is not supported by an enabling disclosure. Applicants respectfully disagree.

Applicants remind the Examiner of MPEP § 2164.01, which states:

> The test of enablement is whether one reasonably skilled in the art could make or use the invention from the disclosures in the patent coupled with information known in the art without undue experimentation.

Applicants submit that practicing the claimed invention would not require experimentation that would be considered to be "undue". Throughout the specification, Applicants provide specific guidance as to the specific steps of the claimed method (see pages 6-18). Further, Applicants provide specific guidance as to the PCR conditions (see top of page 17).

In making this rejection, the Examiner alleges that "of the four examples, only Example 3 relates directly to the claimed method." The Examiner further alleges that "Example 3 consists of but three sentences, and does not set forth any reaction conditions or starting materials."

Even setting aside for a moment the fact that MPEP states in §2164.02:

> The specification need not contain an example if the invention is otherwise disclosed in such manner that one skilled in the art will be able to practice it without an undue amount of experimentation.

Applicants note that the Examiner's aforementioned allegations are false. First, Applicants direct the Examiner's attention to pages 27-28 of the present application. Example 3 is

clearly not only the three sentences on page 27, but also includes the Table and additional description on page 28. On page 28, a pair of primers (SEQ ID NOs: 9 and 10), the template for PCR (yeast total DNA), and the reaction conditions for PCR (the same as in Comparative Example 1) are all clearly described. Further, not only does Example 3 relate to the claimed invention, but also Example 2 directly relates to the claimed method (e.g., Claim 2 is directed to SEQ ID NO: 7 and 8, and so is Example 2). Thus, despite being under no obligation to provide working examples, Applicants have provided two relevant examples by which to illustrate the claimed invention.

In attempting to provide summaries as to the state of the art, the Examiner cites four U.S. pre-grant publications. However, what the Examiner overlooks in this citation is their relevance, or lack thereof, to the claimed invention. Specifically, it is noted that the genome of yeast is approximately 1.25×10^7 bp. Therefore, the minimal polynucleotide sequence that can be considered to be a statistically unique sequence in the yeast genome is a twelve-mer. The probability of a twelve-mer being randomly repeated is calculated as 4^{12}. Thus, the corresponding frequency is one occurrence every 1.7×10^7 bp. In Claim 1, the first primer is SEQ ID NO: 7 (i.e., a 20-mer with an estimated frequency of once very 1.0×10^{12} bp), while the second primer in the pair ranges from 15 (estimated frequency of once very 1.0×10^9 bp) to 30 (estimated frequency of once very 1.0×10^{18} bp) nucleotides. In Claim 2, the first primer is defined as SEQ ID NO: 7 and the second primer is defined as SEQ ID NO: 8 (both 20-mers with an estimated frequency of once very 1.0×10^{12} bp). In view of the foregoing, Applicants submit that the primers of the present invention represent statistically unique sequences on the yeast genome and, thus, improper or false priming is of no relevance.

Further, one of the references cited by the Examiner refers to the problems with multiplex-PCR. However, the presently claimed invention does not encompass multiplex-

PCR. The presently claimed invention clearly recites "a pair of primers" meaning that only two are present. As stated above, in Claim 1 the first primer is SEQ ID NO: 7, while the second primer in the pair ranges from 15 to 30 nucleotides that is complementary to a base sequence of chromosome IX of *Saccharomyces cerevisiae* located downstream from a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, and SEQ ID NO: 6. In Claim 2, the first primer is defined as SEQ ID NO: 7 and the second primer is defined as SEQ ID NO: 8.

Applicants submit that, with the present specification in hand, discrimination between bottom-fermenting yeast and wild yeast would require nothing more than routine experimentation. As such, Applicants submit that Claims 5-8 are fully enabled within the context of 35 U.S.C. §112, first paragraph.

Withdrawal of this ground of rejection is requested.

The rejection of Claims 1-3 under 35 U.S.C. §112, second paragraph, is obviated by amendment.

Applicants have amended the preamble of the claims to specify that the claims relate to a method of differentiating bottom-fermenting yeast from wild yeast. Accordingly, Applicants submit that this ground of rejection is now moot.

Withdrawal of this ground of rejection is requested.

Applicants submit that the present application is now in condition for allowance.

Early notification of such action is earnestly solicited.

Respectfully submitted,

OBLON, SPIVAK, McCLELLAND,
MAIER & NEUSTADT, P.C.
Norman F. Oblon

Vincent K. Shier, Ph.D.
Registration No. 50,552

Customer Number
22850

Tel: (703) 413-3000
Fax: (703) 413-2220
(OSMMN 08/03)